

SEQUENCE LISTING

<110> Becker, Kenneth David
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 Tanzi, Rudolph E.
 Bertram, Lars
 Saunders, Aleister J.
 Mullin, Kristina M.
 Sampson, Andrew Johnson
 Blacker, Deborah Lynne

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caatgcttgt	taatggttaa	tataggcagg	gcgaatacta	ctttgtact	tttaaagtct	40140
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<210> 469

<211> 720

<212> DNA

<213> Homo sapiens

<220>

<221> allele

<222> 30,57,85,243,250,377,512,531,555,561,672

<223> N is any

<400> 469

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gcggagaaca	tcgcggtcac	ctccgggggtg	gtgcgcaagg	aggacttgag	gccatctgcc	360
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<210> 470

<211> 3279

<212> DNA

<213> Homo sapiens

<400> 470

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accacggata	agtcatcagc	agcacttgat	gtgcacatag	gttcattgtc	ggatcctcca	360
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<210> 471
 <211> 4910
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (143)...(3313)
 <223> Nucleic acid sequence encoding KNSL1

<400> 471

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tgattttttg	gcggggaccg	tc atg gcg	tcg cag cca	aat tcg tct	gcg aag	172
		Met Ala Ser Gln	Pro Asn Ser Ser	Ala Lys		
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aag aaa gag gag aag ggg aag aac atc cag gtg gtg gtg aga tgc aga	220					
Lys Lys Glu Glu Lys Gly Lys Asn Ile Gln Val Val Val Arg Cys Arg		15	20	25		
cca ttt aat ttg gca gag cgg aaa gct agc gcc cat tca ata gta gaa	268					
Pro Phe Asn Leu Ala Glu Arg Lys Ala Ser Ala His Ser Ile Val Glu		30	35	40		
tgt gat cct gta cga aaa gaa gtt agt gta cga act gga gga ttg gct	316					
Cys Asp Pro Val Arg Lys Glu Val Ser Val Arg Thr Gly Gly Leu Ala		45	50	55		
gac aag agc tca agg aaa aca tac act ttt gat atg gtg ttt gga gca	364					
Asp Lys Ser Ser Arg Lys Thr Tyr Thr Phe Asp Met Val Phe Gly Ala		60	65	70		
tct act aaa cag att gat gtt tac cga agt gtt gtt tgt cca att ctg	412					
Ser Thr Lys Gln Ile Asp Val Tyr Arg Ser Val Val Cys Pro Ile Leu		75	80	85	90	
gat gaa gtt att atg ggc tat aat tgc act atc ttt gcg tat ggc caa	460					
Asp Glu Val Ile Met Gly Tyr Asn Cys Thr Ile Phe Ala Tyr Gly Gln		95	100	105		
act ggc act gga aaa act ttt aca atg gaa ggt gaa agg tca cct aat	508					
Thr Gly Thr Gly Lys Thr Phe Thr Met Glu Gly Glu Arg Ser Pro Asn		110	115	120		
gaa gag tat acc tgg gaa gag gat ccc ttg gct ggt ata att cca cgt	556					
Glu Glu Tyr Thr Trp Glu Glu Asp Pro Leu Ala Gly Ile Ile Pro Arg		125	130	135		
acc ctt cat caa att ttt gag aaa ctt act gat aat ggt act gaa ttt	604					
Thr Leu His Gln Ile Phe Glu Lys Leu Thr Asp Asn Gly Thr Glu Phe		140	145	150		
tca gtc aaa gtg tct ctg ttg gag atc tat aat gaa gag ctt ttt gat	652					
Ser Val Lys Val Ser Leu Leu Glu Ile Tyr Asn Glu Glu Leu Phe Asp		155	160	165	170	
ctt ctt aat cca tca tct gat gtt tct gag aga cta cag atg ttt gat	700					
Leu Leu Asn Pro Ser Ser Asp Val Ser Glu Arg Leu Gln Met Phe Asp		175	180	185		
gat ccc cgt aac aag aga gga gtg ata att aaa ggt tta gaa gaa att	748					
Asp Pro Arg Asn Lys Arg Gly Val Ile Ile Lys Gly Leu Glu Glu Ile		190	195	200		
aca gta cac aac aag gat gaa gtc tat caa att tta gaa aag ggg gca	796					
Thr Val His Asn Lys Asp Glu Val Tyr Gln Ile Leu Glu Lys Gly Ala		205	210	215		
gca aaa agg aca act gca gct act ctg atg aat gca tac tct agt cgt	844					
Ala Lys Arg Thr Thr Ala Ala Thr Leu Met Asn Ala Tyr Ser Ser Arg		220	225	230		
tcc cac tca gtt ttc tct gtt aca ata cat atg aaa gaa act acg att	892					
Ser His Ser Val Phe Ser Val Thr Ile His Met Lys Glu Thr Thr Ile		235	240	245	250	
gat gga gaa gag ctt gtt aaa atc gga aag ttg aac ttg gtt gat ctt	940					

Asp	Gly	Glu	Glu	Leu	Val	Lys	Ile	Gly	Lys	Leu	Asn	Leu	Val	Asp	Leu	
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gca	gga	agt	gaa	aac	att	ggc	cgt	tct	gga	gct	gtt	gat	aag	aga	gct	988
Ala	Gly	Ser	Glu	Asn	Ile	Gly	Arg	Ser	Gly	Ala	Val	Asp	Lys	Arg	Ala	
			270					275					280			
cgg	gaa	gct	gga	aat	ata	aat	caa	tcc	ctg	ttg	act	ttg	gga	agg	gtc	1036
Arg	Glu	Ala	Gly	Asn	Ile	Asn	Gln	Ser	Leu	Leu	Thr	Leu	Gly	Arg	Val	
		285					290					295				
att	act	gcc	ctt	gta	gaa	aga	aca	cct	cat	gtt	cct	tat	cga	gaa	tct	1084
Ile	Thr	Ala	Leu	Val	Glu	Arg	Thr	Pro	His	Val	Pro	Tyr	Arg	Glu	Ser	
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aaa	cta	act	aga	atc	ctc	cag	gat	tct	ctt	gga	ggg	cgt	aca	aga	aca	1132
Lys	Leu	Thr	Arg	Ile	Leu	Gln	Asp	Ser	Leu	Gly	Gly	Arg	Thr	Arg	Thr	
315					320					325					330	
tct	ata	att	gca	aca	att	tct	cct	gca	tct	ctc	aat	ctt	gag	gaa	act	1180
Ser	Ile	Ile	Ala	Thr	Ile	Ser	Pro	Ala	Ser	Leu	Asn	Leu	Glu	Glu	Thr	
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ctg	agt	aca	ttg	gaa	tat	gct	cat	aga	gca	aag	aac	ata	ttg	aat	aag	1228
Leu	Ser	Thr	Leu	Glu	Tyr	Ala	His	Arg	Ala	Lys	Asn	Ile	Leu	Asn	Lys	
			350					355					360			
cct	gaa	gtg	aat	cag	aaa	ctc	acc	aaa	aaa	gct	ctt	att	aag	gag	tat	1276
Pro	Glu	Val	Asn	Gln	Lys	Leu	Thr	Lys	Lys	Ala	Leu	Ile	Lys	Glu	Tyr	
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acg	gag	gag	ata	gaa	cgt	tta	aaa	cga	gat	ctt	gct	gca	gcc	cgt	gag	1324
Thr	Glu	Glu	Ile	Glu	Arg	Leu	Lys	Arg	Asp	Leu	Ala	Ala	Ala	Arg	Glu	
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aaa	aat	gga	gtg	tat	att	tct	gaa	gaa	aat	ttt	aga	gtc	atg	agt	gga	1372
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Lys	Leu	Thr	Val	Gln	Glu	Glu	Gln	Ile	Val	Glu	Leu	Ile	Glu	Lys	Ile	
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ggg	gct	gtt	gag	gag	gag	ctg	aat	agg	gtt	aca	gag	ttg	ttt	atg	gat	1468
Gly	Ala	Val	Glu	Glu	Glu	Leu	Asn	Arg	Val	Thr	Glu	Leu	Phe	Met	Asp	
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Asn	Lys	Asn	Glu	Leu	Asp	Gln	Cys	Lys	Ser	Asp	Leu	Gln	Asn	Lys	Thr	
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caa	gaa	ctt	gaa	acc	act	caa	aaa	cat	ttg	caa	gaa	act	aaa	tta	caa	1564
Gln	Glu	Leu	Glu	Thr	Thr	Gln	Lys	His	Leu	Gln	Glu	Thr	Lys	Leu	Gln	
	460					465					470					
ctt	gtt	aaa	gaa	gaa	tat	atc	aca	tca	gct	ttg	gaa	agt	act	gag	gag	1612
Leu	Val	Lys	Glu	Glu	Tyr	Ile	Thr	Ser	Ala	Leu	Glu	Ser	Thr	Glu	Glu	
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Lys	Leu	His	Asp	Ala	Ala	Ser	Lys	Leu	Leu	Asn	Thr	Val	Glu	Glu	Thr	
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Thr	Lys	Asp	Val	Ser	Gly	Leu	His	Ser	Lys	Leu	Asp	Arg	Lys	Lys	Ala	
			510					515					520			

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Val	Asp	Gln	His	Asn	Ala	Glu	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Asn	Leu	
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Asn	Ser	Leu	Phe	Asn	Asn	Met	Glu	Glu	Leu	Ile	Lys	Asp	Gly	Ser	Ser	
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Lys	Gln	Lys	Ala	Met	Leu	Glu	Val	His	Lys	Thr	Leu	Phe	Gly	Asn	Leu	
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Leu	Ser	Ser	Ser	Val	Ser	Ala	Leu	Asp	Thr	Ile	Thr	Thr	Val	Ala	Leu	
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Gly	Ser	Leu	Thr	Ser	Ile	Pro	Glu	Asn	Val	Ser	Thr	His	Val	Ser	Gln	
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Ile	Phe	Asn	Met	Ile	Leu	Lys	Glu	Gln	Ser	Leu	Ala	Ala	Glu	Ser	Lys	
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Cys	Asn	Asn	Leu	His	Glu	Leu	Gln	Glu	Asn	Thr	Ile	Cys	Ser	Leu	Val	
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Glu	Ser	Gln	Lys	Gln	Cys	Gly	Asn	Leu	Thr	Glu	Asp	Leu	Lys	Thr	Ile	
	700					705					710					
aag	cag	acc	cat	tcc	cag	gaa	ctt	tgc	aag	tta	atg	aat	ctt	tgg	aca	2332
Lys	Gln	Thr	His	Ser	Gln	Glu	Leu	Cys	Lys	Leu	Met	Asn	Leu	Trp	Thr	
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Glu	Arg	Phe	Cys	Ala	Leu	Glu	Glu	Lys	Cys	Glu	Asn	Ile	Gln	Lys	Pro	
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ctt	agt	agt	gtc	cag	gaa	aat	ata	cag	cag	aaa	tct	aag	gat	ata	gtc	2428
Leu	Ser	Ser	Val	Gln	Glu	Asn	Ile	Gln	Gln	Lys	Ser	Lys	Asp	Ile	Val	
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Asn	Lys	Met	Thr	Phe	His	Ser	Gln	Lys	Phe	Cys	Ala	Asp	Ser	Asp	Gly	
		765					770					775				
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Phe	Ser	Gln	Glu	Leu	Arg	Asn	Phe	Asn	Gln	Glu	Gly	Thr	Lys	Leu	Val	
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Glu Glu Ser Val Lys His Ser Asp Lys Leu Asn Gly Asn Leu Glu Lys	
795 800 805 810	
ata tct caa gag act gaa cag aga tgt gaa tct ctg aac aca aga aca	2620
Ile Ser Gln Glu Thr Glu Gln Arg Cys Glu Ser Leu Asn Thr Arg Thr	
815 820 825	
gtt tat ttt tct gaa cag tgg gta tct tcc tta aat gaa agg gaa cag	2668
Val Tyr Phe Ser Glu Gln Trp Val Ser Ser Leu Asn Glu Arg Glu Gln	
830 835 840	
gaa ctt cac aac tta ttg gag gtt gta agc caa tgt tgt gag gct tca	2716
Glu Leu His Asn Leu Leu Glu Val Val Ser Gln Cys Cys Glu Ala Ser	
845 850 855	
agt tca gac atc act gag aaa tca gat gga dgt aag gca gct cat gag	2764
Ser Ser Asp Ile Thr Glu Lys Ser Asp Gly Xaa Lys Ala Ala His Glu	
860 865 870	
aaa cag cat aac att ttt ctt gat cag atg act att gat gaa gat aaa	2812
Lys Gln His Asn Ile Phe Leu Asp Gln Met Thr Ile Asp Glu Asp Lys	
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Gln Pro Glu Leu Leu Met Met Leu Asn Cys Ser Glu Asn Asn Lys Glu	
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Cys Ser Ser Ile Gly Gly Val Pro Phe Phe Gln His Lys Lys Ser His	
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Val Glu Glu Thr Thr Glu His Leu Val Thr Lys Ser Arg Leu Pro Leu	
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Arg Ala Gln Ile Asn Leu *	

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<211> 1056

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> 869

<223> Xaa = any amino acid

<400> 472

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35 40 45
Glu Val Ser Val Arg Thr Gly Gly Leu Ala Asp Lys Ser Ser Arg Lys
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Thr Tyr Thr Phe Asp Met Val Phe Gly Ala Ser Thr Lys Gln Ile Asp
65 70 75 80
Val Tyr Arg Ser Val Val Cys Pro Ile Leu Asp Glu Val Ile Met Gly
85 90 95
Tyr Asn Cys Thr Ile Phe Ala Tyr Gly Gln Thr Gly Thr Gly Lys Thr
100 105 110
Phe Thr Met Glu Gly Glu Arg Ser Pro Asn Glu Glu Tyr Thr Trp Glu
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Glu Asp Pro Leu Ala Gly Ile Ile Pro Arg Thr Leu His Gln Ile Phe
130 135 140
Glu Lys Leu Thr Asp Asn Gly Thr Glu Phe Ser Val Lys Val Ser Leu
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Leu Glu Ile Tyr Asn Glu Glu Leu Phe Asp Leu Leu Asn Pro Ser Ser
165 170 175
Asp Val Ser Glu Arg Leu Gln Met Phe Asp Asp Pro Arg Asn Lys Arg
180 185 190
Gly Val Ile Ile Lys Gly Leu Glu Ile Thr Val His Asn Lys Asp
195 200 205

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Ile	Thr	Ser	Ala	Leu	Glu	Ser	Thr	Glu	Glu	Lys	Leu	His	Asp	Ala	Ala
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Ser	Lys	Leu	Leu	Asn	Thr	Val	Glu	Glu	Thr	Thr	Lys	Asp	Val	Ser	Gly
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<222> (6)...(3176)

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Glu Arg Lys Ala Ser Ala His Ser Ile Val Glu Cys Asp Pro Val Arg

35 40 45

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Lys Glu Val Ser Val Arg Thr Gly Gly Leu Ala Asp Lys Ser Ser Arg

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Tyr Ala His Arg Ala	Lys Asn Ile Leu Asn	Lys Pro Glu Val Asn	Gln				
	355	360	365				
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Lys Leu Thr Lys Lys	Ala Leu Ile Lys Glu	Tyr Thr Glu Glu Ile	Glu				
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Glu Leu Asn Arg Val	Thr Glu Leu Phe Met	Asp Asn Lys Asn Glu	Leu				
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Ala Ser Lys Leu Leu	Asn Thr Val Glu Glu	Thr Thr Lys Asp Val	Ser				
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Gly Leu His Ser Lys	Leu Asp Arg Lys Lys	Ala Val Asp Gln His	Asn				
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Asn Met Glu Glu Leu	Ile Lys Asp Gly Ser	Ser Lys Gln Lys Ala	Met				
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Ser Ala Leu Asp Thr	Ile Thr Thr Val Ala	Leu Gly Ser Leu Thr	Ser				
	580	585	590				
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Ile	Pro	Glu	Asn	Val	Ser	Thr	His	Val	Ser	Gln	Ile	Phe	Asn	Met	Ile	
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cta	aaa	gaa	caa	tca	tta	gca	gca	gaa	agt	aaa	act	gta	cta	cag	gaa	1874
Leu	Lys	Glu	Gln	Ser	Leu	Ala	Ala	Glu	Ser	Lys	Thr	Val	Leu	Gln	Glu	
		610				615						620				
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Leu	Ile	Asn	Val	Leu	Lys	Thr	Asp	Leu	Leu	Ser	Ser	Leu	Glu	Met	Ile	
	625					630					635					
tta	tcc	cca	act	gtg	gtg	tct	ata	ctg	aaa	atc	aat	agt	caa	cta	aag	1970
Leu	Ser	Pro	Thr	Val	Val	Ser	Ile	Leu	Lys	Ile	Asn	Ser	Gln	Leu	Lys	
640					645					650					655	
cat	att	ttc	aag	act	tca	ttg	aca	gtg	gcc	gat	aag	ata	gaa	gat	caa	2018
His	Ile	Phe	Lys	Thr	Ser	Leu	Thr	Val	Ala	Asp	Lys	Ile	Glu	Asp	Gln	
				660					665					670		
aaa	aag	gaa	cta	gat	ggc	ttt	ctc	agt	ata	ctg	tgt	aac	aat	cta	cat	2066
Lys	Lys	Glu	Leu	Asp	Gly	Phe	Leu	Ser	Ile	Leu	Cys	Asn	Asn	Leu	His	
			675					680					685			
gaa	cta	caa	gaa	aat	acc	att	tgt	tcc	ttg	gtt	gag	tca	caa	aag	caa	2114
Glu	Leu	Gln	Glu	Asn	Thr	Ile	Cys	Ser	Leu	Val	Glu	Ser	Gln	Lys	Gln	
		690					695					700				
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Cys	Gly	Asn	Leu	Thr	Glu	Asp	Leu	Lys	Thr	Ile	Lys	Gln	Thr	His	Ser	
	705					710					715					
cag	gaa	ctt	tgc	aag	tta	atg	aat	ctt	tgg	aca	gag	aga	ttc	tgt	gct	2210
Gln	Glu	Leu	Cys	Lys	Leu	Met	Asn	Leu	Trp	Thr	Glu	Arg	Phe	Cys	Ala	
720					725				730						735	
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His	Ser	Asp	Lys	Leu	Asn	Gly	Asn	Leu	Glu	Lys	Ile	Ser	Gln	Glu	Thr	
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gaa	cag	aga	tgt	gaa	tct	ctg	aac	aca	aga	aca	gtt	tat	ttt	tct	gaa	2498
Glu	Gln	Arg	Cys	Glu	Ser	Leu	Asn	Thr	Arg	Thr	Val	Tyr	Phe	Ser	Glu	
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cag	tgg	gta	tct	tcc	tta	aat	gaa	agg	gaa	cag	gaa	ctt	cac	aac	tta	2546
Gln	Trp	Val	Ser	Ser	Leu	Asn	Glu	Arg	Glu	Gln	Glu	Leu	His	Asn	Leu	
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Leu	Glu	Val	Val	Ser	Gln	Cys	Cys	Glu	Ala	Ser	Ser	Ser	Asp	Ile	Thr	
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Glu	Lys	Ser	Asp	Gly	Xaa	Lys	Ala	Ala	His	Glu	Lys	Gln	His	Asn	Ile	
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Phe	Leu	Asp	Gln	Met	Thr	Ile	Asp	Glu	Asp	Lys	Leu	Ile	Ala	Gln	Asn	
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Leu	Glu	Leu	Asn	Glu	Thr	Ile	Lys	Ile	Gly	Leu	Thr	Lys	Leu	Asn	Cys	
				900					905					910		
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Phe	Leu	Glu	Gln	Asp	Leu	Lys	Leu	Asp	Ile	Pro	Thr	Gly	Thr	Thr	Pro	
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Arg	Glu	His	Leu	Leu	Asp	Gln	Leu	Lys	Arg	Lys	Gln	Pro	Glu	Leu	Leu	
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Met	Met	Leu	Asn	Cys	Ser	Glu	Asn	Asn	Lys	Glu	Glu	Thr	Ile	Pro	Asp	
	960				965					970					975	
gtg	gat	gta	gaa	gag	gca	gtt	ctg	ggg	cag	tat	act	gaa	gaa	cct	cta	2978
Val	Asp	Val	Glu	Glu	Ala	Val	Leu	Gly	Gln	Tyr	Thr	Glu	Glu	Pro	Leu	
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Glu	His	Leu	Val	Thr	Lys	Ser	Arg	Leu	Pro	Leu	Arg	Ala	Gln	Ile	Asn	
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Leu	*															
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<212> PRT

<213> Homo sapiens

<220>
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<400> 474

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Arg	Lys	Ala	Ser	Ala	His	Ser	Ile	Val	Glu	Cys	Asp	Pro	Val	Arg	Lys
		35					40					45			
Glu	Val	Ser	Val	Arg	Thr	Gly	Gly	Leu	Ala	Asp	Lys	Ser	Ser	Arg	Lys
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Thr	Tyr	Thr	Phe	Asp	Met	Val	Phe	Gly	Ala	Ser	Thr	Lys	Gln	Ile	Asp
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Val	Tyr	Arg	Ser	Val	Val	Cys	Pro	Ile	Leu	Asp	Glu	Val	Ile	Met	Gly
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Tyr	Asn	Cys	Thr	Ile	Phe	Ala	Tyr	Gly	Gln	Thr	Gly	Thr	Gly	Lys	Thr
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Phe	Thr	Met	Glu	Gly	Glu	Arg	Ser	Pro	Asn	Glu	Glu	Tyr	Thr	Trp	Glu
		115					120					125			
Glu	Asp	Pro	Leu	Ala	Gly	Ile	Ile	Pro	Arg	Thr	Leu	His	Gln	Ile	Phe
	130					135					140				
Glu	Lys	Leu	Thr	Asp	Asn	Gly	Thr	Glu	Phe	Ser	Val	Lys	Val	Ser	Leu
145					150					155					160
Leu	Glu	Ile	Tyr	Asn	Glu	Glu	Leu	Phe	Asp	Leu	Leu	Asn	Pro	Ser	Ser
			165						170					175	
Asp	Val	Ser	Glu	Arg	Leu	Gln	Met	Phe	Asp	Asp	Pro	Arg	Asn	Lys	Arg
			180					185					190		
Gly	Val	Ile	Ile	Lys	Gly	Leu	Glu	Glu	Ile	Thr	Val	His	Asn	Lys	Asp
	195					200						205			
Glu	Val	Tyr	Gln	Ile	Leu	Glu	Lys	Gly	Ala	Ala	Lys	Arg	Thr	Thr	Ala
	210					215					220				
Ala	Thr	Leu	Met	Asn	Ala	Tyr	Ser	Ser	Arg	Ser	His	Ser	Val	Phe	Ser
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Val	Thr	Ile	His	Met	Lys	Glu	Thr	Thr	Ile	Asp	Gly	Glu	Glu	Leu	Val
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Lys	Ile	Gly	Lys	Leu	Asn	Leu	Val	Asp	Leu	Ala	Gly	Ser	Glu	Asn	Ile
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	275					280						285			
Asn	Gln	Ser	Leu	Leu	Thr	Leu	Gly	Arg	Val	Ile	Thr	Ala	Leu	Val	Glu
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Arg	Thr	Pro	His	Val	Pro	Tyr	Arg	Glu	Ser	Lys	Leu	Thr	Arg	Ile	Leu
305				310						315					320
Gln	Asp	Ser	Leu	Gly	Gly	Arg	Thr	Arg	Thr	Ser	Ile	Ile	Ala	Thr	Ile
			325						330					335	
Ser	Pro	Ala	Ser	Leu	Asn	Leu	Glu	Glu	Thr	Leu	Ser	Thr	Leu	Glu	Tyr
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Ala	His	Arg	Ala	Lys	Asn	Ile	Leu	Asn	Lys	Pro	Glu	Val	Asn	Gln	Lys
		355					360					365			
Leu	Thr	Lys	Lys	Ala	Leu	Ile	Lys	Glu	Tyr	Thr	Glu	Glu	Ile	Glu	Arg
	370					375					380				
Leu	Lys	Arg	Asp	Leu	Ala	Ala	Ala	Arg	Glu	Lys	Asn	Gly	Val	Tyr	Ile
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Ser	Glu	Glu	Asn	Phe	Arg	Val	Met	Ser	Gly	Lys	Leu	Thr	Val	Gln	Glu
			405						410					415	
Glu	Gln	Ile	Val	Glu	Leu	Ile	Glu	Lys	Ile	Gly	Ala	Val	Glu	Glu	Glu
		420					425						430		
Leu	Asn	Arg	Val	Thr	Glu	Leu	Phe	Met	Asp	Asn	Lys	Asn	Glu	Leu	Asp
	435						440					445			
Gln	Cys	Lys	Ser	Asp	Leu	Gln	Asn	Lys	Thr	Gln	Glu	Leu	Glu	Thr	Thr
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Gln	Lys	His	Leu	Gln	Glu	Thr	Lys	Leu	Gln	Leu	Val	Lys	Glu	Glu	Tyr
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Ile	Thr	Ser	Ala	Leu	Glu	Ser	Thr	Glu	Glu	Lys	Leu	His	Asp	Ala	Ala

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			500					505					510				
Leu	His	Ser	Lys	Leu	Asp	Arg	Lys	Lys	Ala	Val	Asp	Gln	His	Asn	Ala		
		515					520					525					
Glu	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Asn	Leu	Asn	Ser	Leu	Phe	Asn	Asn		
	530					535					540						
Met	Glu	Glu	Leu	Ile	Lys	Asp	Gly	Ser	Ser	Lys	Gln	Lys	Ala	Met	Leu		
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Glu	Val	His	Lys	Thr	Leu	Phe	Gly	Asn	Leu	Leu	Ser	Ser	Ser	Val	Ser		
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Ala	Leu	Asp	Thr	Ile	Thr	Thr	Val	Ala	Leu	Gly	Ser	Leu	Thr	Ser	Ile		
			580					585					590				
Pro	Glu	Asn	Val	Ser	Thr	His	Val	Ser	Gln	Ile	Phe	Asn	Met	Ile	Leu		
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Lys	Glu	Gln	Ser	Leu	Ala	Ala	Glu	Ser	Lys	Thr	Val	Leu	Gln	Glu	Leu		
	610					615					620						
Ile	Asn	Val	Leu	Lys	Thr	Asp	Leu	Leu	Ser	Ser	Leu	Glu	Met	Ile	Leu		
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Ile	Phe	Lys	Thr	Ser	Leu	Thr	Val	Ala	Asp	Lys	Ile	Glu	Asp	Gln	Lys		
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Lys	Glu	Leu	Asp	Gly	Phe	Leu	Ser	Ile	Leu	Cys	Asn	Asn	Leu	His	Glu		
	675					680					685						
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Glu	Glu	Lys	Cys	Glu	Asn	Ile	Gln	Lys	Pro	Leu	Ser	Ser	Val	Gln	Glu		
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Asn	Ile	Gln	Gln	Lys	Ser	Lys	Asp	Ile	Val	Asn	Lys	Met	Thr	Phe	His		
	755						760					765					
Ser	Gln	Lys	Phe	Cys	Ala	Asp	Ser	Asp	Gly	Phe	Ser	Gln	Glu	Leu	Arg		
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Trp	Val	Ser	Ser	Leu	Asn	Glu	Arg	Glu	Gln	Glu	Leu	His	Asn	Leu	Leu		
	835						840						845				
Glu	Val	Val	Ser	Gln	Cys	Cys	Glu	Ala	Ser	Ser	Ser	Asp	Ile	Thr	Glu		
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Lys	Ser	Asp	Gly	Xaa	Lys	Ala	Ala	His	Glu	Lys	Gln	His	Asn	Ile	Phe		
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Leu	Glu	Gln	Asp	Leu	Lys	Leu	Asp	Ile	Pro	Thr	Gly	Thr	Thr	Pro	Gln		
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Glu	His	Leu	Leu	Asp	Gln	Leu	Lys	Arg	Lys	Gln	Pro	Glu	Leu	Leu	Met		
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Arg Gly Ile Asn Thr Leu Glu Arg Ser Lys Val Glu Glu Thr Thr Glu
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<220>
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 Met Ala Ser Gln Pro Asn Ser Ser
 1 5

gcg aag aag aaa gag gag aag ggg aag aac atc cag gtg gtg gtg aga 162
 Ala Lys Lys Lys Glu Glu Lys Gly Lys Asn Ile Gln Val Val Val Arg
 10 15 20

tgc aga cca ttt aat ttg gca gag cgg aaa gct agc gcc cat tca ata 210
 Cys Arg Pro Phe Asn Leu Ala Glu Arg Lys Ala Ser Ala His Ser Ile
 25 30 35 40

gta gaa tgt gat cct gta cga aaa gaa gtt agt gta cga act gga gga 258
 Val Glu Cys Asp Pro Val Arg Lys Glu Val Ser Val Arg Thr Gly Gly
 45 50 55

ttg gct gac aag agc tca agg aaa aca tac act ttt gat atg gtg ttt 306
 Leu Ala Asp Lys Ser Ser Arg Lys Thr Tyr Thr Phe Asp Met Val Phe
 60 65 70

gga gca tct act aaa cag att gat gtt tac cga agt gtt gtt tgt cca 354
 Gly Ala Ser Thr Lys Gln Ile Asp Val Tyr Arg Ser Val Val Cys Pro
 75 80 85

att ctg gat gaa gtt att atg ggc tat aat tgc act atc ttt gcg tat 402
 Ile Leu Asp Glu Val Ile Met Gly Tyr Asn Cys Thr Ile Phe Ala Tyr
 90 95 100

ggc caa act ggc act gga aaa act ttt aca atg gaa ggt gaa agg tca 450
 Gly Gln Thr Gly Thr Gly Lys Thr Phe Thr Met Glu Gly Glu Arg Ser
 105 110 115 120

cct aat gaa gag tat acc tgg gaa gag gat ccc ttg gct ggt ata att 498
 Pro Asn Glu Glu Tyr Thr Trp Glu Glu Asp Pro Leu Ala Gly Ile Ile
 125 130 135

cca cgt acc ctt cat caa att ttt gag aaa ctt act gat aat ggt act 546
 Pro Arg Thr Leu His Gln Ile Phe Glu Lys Leu Thr Asp Asn Gly Thr
 140 145 150

gaa ttt tca gtc aaa gtg tct ctg ttg gag atc tat aat gaa gag ctt 594
 Glu Phe Ser Val Lys Val Ser Leu Leu Glu Ile Tyr Asn Glu Glu Leu
 155 160 165

ttt gat ctt ctt aat cca tca tct gat gtt tct gag aga cta cag atg 642
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Phe 185	Asp	Asp	Pro	Arg	Asn 190	Lys	Arg	Gly	Val	Ile 195	Ile	Lys	Gly	Leu	Glu 200	
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agt Ser	cgt Arg	tcc Ser 235	cac His	tca Ser	gtt Val	ttc Phe	tct Ser 240	gtt Val	aca Thr	ata Ile	cat His	atg Met 245	aaa Lys	gaa Glu	act Thr	834
acg Thr	att Ile 250	gat Asp	gga Gly	gaa Glu	gag Glu	ctt Leu 255	gtt Val	aaa Lys	atc Ile	gga Gly 260	aag Lys	ttg Leu	aac Asn	ttg Leu	gtt Val	882
gat Asp 265	ctt Leu	gca Ala	gga Gly	agt Ser	gaa Glu 270	aac Asn	att Ile	ggc Gly	cgt Arg	tct Ser 275	gga Gly	gct Ala	gtt Val	gat Asp	aag Lys 280	930
aga Arg	gct Ala	cgg Arg	gaa Glu	gct Ala 285	gga Gly	aat Asn	ata Ile	aat Asn	caa Gln 290	tcc Ser	ctg Leu	ttg Leu	act Thr	ttg Leu 295	gga Gly	978
agg Arg	gtc Val	att Ile	act Thr 300	gcc Ala	ctt Leu	gta Val	gaa Glu	aga Arg 305	aca Thr	cct Pro	cat His	gtt Val 310	cct Pro	tat Tyr	cga Arg	1026
gaa Glu	tct Ser	aaa Lys 315	cta Leu	act Thr	aga Arg	atc Ile 320	ctc Leu	cag Gln	gat Asp	tct Ser	ctt Leu	gga Gly 325	ggg Gly	cgt Arg	aca Thr	1074
aga Arg	aca Thr 330	tct Ser	ata Ile	att Ile	gca Ala 335	aca Thr	att Ile	tct Ser	cct Pro	gca Ala 340	tct Ser	ctc Leu	aat Asn	ctt Leu	gag Glu	1122
gaa Glu 345	act Thr	ctg Leu	agt Ser	aca Thr	ttg Leu 350	gaa Glu	tat Tyr	gct Ala	cat His	aga Arg 355	gca Ala	aag Lys	aac Asn	ata Ile	ttg Leu 360	1170
aat Asn	aag Lys	cct Pro	gaa Glu	gtg Val 365	aat Asn	cag Gln	aaa Lys	ctc Leu	acc Thr 370	aaa Lys	aaa Lys	gct Ala	ctt Leu	att Ile 375	aag Lys	1218
gag Glu	tat Tyr	acg Thr	gag Glu	gag Glu	ata Ile	gaa Glu	cgt Arg	tta Leu 385	aaa Lys	cga Arg	gat Asp	ctt Leu	gct Ala 390	gca Ala	gcc Ala	1266
cgt Arg	gag Glu	aaa Lys 395	aat Asn	gga Gly	gtg Val	tat Tyr	att Ile 400	tct Ser	gaa Glu	gaa Glu	aat Asn 405	ttt Phe	aga Arg	gtc Val	atg Met	1314
agt Ser	gga Gly 410	aaa Lys	tta Leu	act Thr	gtt Val	caa Gln 415	gaa Glu	gag Glu	cag Gln	att Ile	gta Val 420	gaa Glu	ttg Leu	att Ile	gaa Glu	1362
aaa Lys 425	att Ile	ggg Gly	gct Ala	gtt Val	gag Glu 430	gag Glu	gag Glu	ctg Leu	aat Asn 435	agg Arg	gtt Val	aca Thr	gag Glu	ttg Leu	ttt Phe 440	1410
atg Met	gat Asp	aat Asn	aaa Lys	aat Asn 445	gaa Glu	ctt Leu	gac Asp	cag Gln	tgt Cys 450	aaa Lys	tct Ser	gac Asp	ctg Leu	caa Gln	aat Asn 455	1458

aaa	aca	caa	gaa	ctt	gaa	acc	act	caa	aaa	cat	ttg	caa	gaa	act	aaa	1506
Lys	Thr	Gln	Glu	Leu	Glu	Thr	Thr	Gln	Lys	His	Leu	Gln	Glu	Thr	Lys	
			460					465					470			
tta	caa	ctt	gtt	aaa	gaa	gaa	tat	atc	aca	tca	gct	ttg	gaa	agt	act	1554
Leu	Gln	Leu	Val	Lys	Glu	Glu	Tyr	Ile	Thr	Ser	Ala	Leu	Glu	Ser	Thr	
		475					480					485				
gag	gag	aaa	ctt	cat	gat	gct	gcc	agc	aag	ctg	ctt	aac	aca	gtt	gaa	1602
Glu	Glu	Lys	Leu	His	Asp	Ala	Ala	Ser	Lys	Leu	Leu	Asn	Thr	Val	Glu	
	490					495					500					
gaa	act	aca	aaa	gat	gta	tct	ggt	ctc	cat	tcc	aaa	ctg	gat	cgt	aag	1650
Glu	Thr	Thr	Lys	Asp	Val	Ser	Gly	Leu	His	Ser	Lys	Leu	Asp	Arg	Lys	
505				510						515					520	
aag	gca	gtt	gac	caa	cac	aat	gca	gaa	gct	cag	gat	att	ttt	ggc	aaa	1698
Lys	Ala	Val	Asp	Gln	His	Asn	Ala	Glu	Ala	Gln	Asp	Ile	Phe	Gly	Lys	
				525					530					535		
aac	ctg	aat	agt	ctg	ttt	aat	aat	atg	gaa	gaa	tta	att	aag	gat	ggc	1746
Asn	Leu	Asn	Ser	Leu	Phe	Asn	Asn	Met	Glu	Glu	Leu	Ile	Lys	Asp	Gly	
			540					545					550			
agc	tca	aag	caa	aag	gcc	atg	cta	gaa	gta	cat	aag	acc	tta	ttt	ggt	1794
Ser	Ser	Lys	Gln	Lys	Ala	Met	Leu	Glu	Val	His	Lys	Thr	Leu	Phe	Gly	
		555					560					565				
aat	ctg	ctg	tct	tcc	agt	gtc	tct	gca	tta	gat	acc	att	act	aca	gta	1842
Asn	Leu	Leu	Ser	Ser	Ser	Val	Ser	Ala	Leu	Asp	Thr	Ile	Thr	Thr	Val	
	570					575					580					
gca	ctt	gga	tct	ctc	aca	tct	att	cca	gaa	aat	gtg	tct	act	cat	gtt	1890
Ala	Leu	Gly	Ser	Leu	Thr	Ser	Ile	Pro	Glu	Asn	Val	Ser	Thr	His	Val	
585				590						595					600	
tct	cag	att	ttt	aat	atg	ata	cta	aaa	gaa	caa	tca	tta	gca	gca	gaa	1938
Ser	Gln	Ile	Phe	Asn	Met	Ile	Leu	Lys	Glu	Gln	Ser	Leu	Ala	Ala	Glu	
				605					610				615			
agt	aaa	act	gta	cta	cag	gaa	ttg	att	aat	gta	ctc	aag	act	gat	ctt	1986
Ser	Lys	Thr	Val	Leu	Gln	Glu	Leu	Ile	Asn	Val	Leu	Lys	Thr	Asp	Leu	
			620				625						630			
cta	agt	tca	ctg	gaa	atg	att	tta	tcc	cca	act	gtg	gtg	tct	ata	ctg	2034
Leu	Ser	Ser	Leu	Glu	Met	Ile	Leu	Ser	Pro	Thr	Val	Val	Ser	Ile	Leu	
		635					640					645				
aaa	atc	aat	agt	caa	cta	aag	cat	att	ttc	aag	act	tca	ttg	aca	gtg	2082
Lys	Ile	Asn	Ser	Gln	Leu	Lys	His	Ile	Phe	Lys	Thr	Ser	Leu	Thr	Val	
	650					655					660					
gcc	gat	aag	ata	gaa	gat	caa	aaa	aag	gaa	cta	gat	ggc	ttt	ctc	agt	2130
Ala	Asp	Lys	Ile	Glu	Asp	Gln	Lys	Lys	Glu	Leu	Asp	Gly	Phe	Leu	Ser	
665				670						675				680		
ata	ctg	tgt	aac	aat	cta	cat	gaa	cta	caa	gaa	aat	acc	att	tgt	tcc	2178
Ile	Leu	Cys	Asn	Asn	Leu	His	Glu	Leu	Gln	Glu	Asn	Thr	Ile	Cys	Ser	
				685					690					695		
ttg	gtt	gag	tca	caa	aag	caa	tgt	gga	aac	cta	act	gaa	gac	ctg	aag	2226
Leu	Val	Glu	Ser	Gln	Lys	Gln	Cys	Gly	Asn	Leu	Thr	Glu	Asp	Leu	Lys	
		700					705						710			
aca	ata	aag	cag	acc	cat	tcc	cag	gaa	ctt	tgc	aag	tta	atg	aat	ctt	2274
Thr	Ile	Lys	Gln	Thr	His	Ser	Gln	Glu	Leu	Cys	Lys	Leu	Met	Asn	Leu	
		715					720						725			

tgg Trp 730	aca Thr	gag Glu	aga Arg	ttc Phe	tgt Cys	gct Ala 735	ttg Leu	gag Glu	gaa Glu	aag Lys 740	tgt Cys	gaa Glu	aat Asn	ata Ile	cag Gln	2322
aaa Lys 745	cca Pro	ctt Leu	agt Ser	agt Ser	gtc Val 750	cag Gln	gaa Glu	aat Asn	ata Ile	cag Gln 755	cag Gln	aaa Lys	tct Ser	aag Lys	gat Asp 760	2370
ata Ile	gtc Val	aac Asn	aaa Lys	atg Met 765	act Thr	ttt Phe	cac His	agt Ser	caa Gln 770	aaa Lys	ttt Phe	tgt Cys	gct Ala 775	gat Asp	tct Ser	2418
gat Asp	ggc Gly	ttc Phe 780	tca Ser	cag Gln	gaa Glu	ctc Leu	aga Arg	aat Asn 785	ttt Phe	aac Asn	caa Gln	gaa Glu	ggg Gly 790	aca Thr	aaa Lys	2466
ttg Leu	gtt Val	gaa Glu 795	gaa Glu	tct Ser	gtg Val	aaa Lys	cac His 800	tct Ser	gat Asp	aaa Lys	ctc Leu	aat Asn 805	ggc Gly	aac Asn	ctg Leu	2514
gaa Glu 810	aaa Lys	ata Ile	tct Ser	caa Gln	gag Glu	act Thr 815	gaa Glu	cag Gln	aga Arg	tgt Cys 820	gaa Glu	tct Ser	ctg Leu	aac Asn	aca Thr	2562
aga Arg 825	aca Thr	gtt Val	tat Tyr	ttt Phe	tct Ser 830	gaa Glu	cag Gln	tgg Trp	gta Val	tct Ser 835	tcc Ser	tta Leu	aat Asn	gaa Glu	agg Arg 840	2610
gaa Glu	cag Gln	gaa Glu	ctt Leu	cac His 845	aac Asn	tta Leu	ttg Leu	gag Glu	gtt Val 850	gta Val	agc Ser	caa Gln	tgt Cys 855	tgt Cys	gag Glu	2658
gct Ala	tca Ser	agt Ser 860	tca Ser	gac Asp	atc Ile	act Thr	gag Glu	aaa Lys 865	tca Ser	gat Asp	gga Gly	dgt Xaa	aag Lys 870	gca Ala	gct Ala	2706
cat His	gag Glu	aaa Lys 875	cag Gln	cat His	aac Asn	att Ile	ttt Phe 880	ctt Leu	gat Asp	cag Gln	atg Met	act Thr 885	att Ile	gat Asp	gaa Glu	2754
gat Asp 890	aaa Lys	ttg Leu	ata Ile	gca Ala	caa Gln	aat Asn 895	cta Leu	gaa Glu	ctt Leu	aat Asn	gaa Glu	acc Thr	ata Ile	aaa Lys	att Ile	2802
ggg Gly 905	ttg Leu	act Thr	aag Lys	ctt Leu	aat Asn 910	tgc Cys	ttt Phe	ctg Leu	gaa Glu	cag Gln 915	gat Asp	ctg Leu	aaa Lys	ctg Leu	gat Asp 920	2850
atc Ile	cca Pro	aca Thr	ggg Gly	acg Thr 925	aca Thr	cca Pro	cag Gln	agg Arg	aaa Lys 930	agt Ser	tat Tyr	tta Leu	tac Tyr 935	cca Pro	tca Ser	2898
aca Thr	ctg Leu	gta Val	aga Arg	act Thr 940	gaa Glu	cca Pro	cgt Arg	gaa Glu	cat His	ctc Leu	ctt Leu	gat Asp	cag Gln 950	ctg Leu	aaa Lys	2946
agg Arg	aaa Lys 955	cag Gln	cct Pro	gag Glu	ctg Leu	tta Leu	atg Met 960	atg Met	cta Leu	aac Asn	tgt Cys 965	tca Ser	gaa Glu	aac Asn	aac Asn	2994
aaa Lys 970	gaa Glu	gag Glu	aca Thr	att Ile	ccg Pro	gat Asp 975	gtg Val	gat Asp	gta Val	gaa Glu	gag Glu	gca Ala	gtt Val	ctg Leu	ggg Gly	3042
cag Gln	tat Tyr	act Thr	gaa Glu	gaa Glu	cct Pro	cta Leu	agt Ser	caa Gln	gag Glu	cca Pro	tct Ser	gta Val	gat Asp	gct Ala	ggg Gly	3090

985	990	995	1000	
gtg gat tgt tca tca att ggc ggg gtt cca ttt ttc cag cat aaa aaa				3138
Val Asp Cys Ser Ser Ile Gly Gly Val Pro Phe Phe Gln His Lys Lys				
	1005	1010	1015	
tca cat gga aaa gac aaa gaa aac aga ggc att aac aca ctg gag agg				3186
Ser His Gly Lys Asp Lys Glu Asn Arg Gly Ile Asn Thr Leu Glu Arg				
	1020	1025	1030	
tct aaa gtg gaa gaa act aca gag cac ttg gtt aca aag agc aga tta				3234
Ser Lys Val Glu Glu Thr Thr Glu His Leu Val Thr Lys Ser Arg Leu				
	1035	1040	1045	
cct ctg cga gcc cag atc aac ctt taa ttcacttggg ggttggcaat				3281
Pro Leu Arg Ala Gln Ile Asn Leu *				
	1050	1055		
tttatttttta aagaaaactt aaaaataaaa cctgaaaccc cagaacttga gccttgtgta				3341
tagatttttaa aagaatatat atatcagccg ggcgcggtgg ctcatgcctg taateccagc				3401
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aacgtggcaa aacctcgtct ctgttaaaaa ttagccgggc gtggtggcac actcctgtaa				3521
tcccagctac tggggaggct gaggcacgag aatcacttga acccaggaag cgggggttgca				3581
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cccatttttc tgtcatccct atagttcact ttgtattaaa ttgggtttca tttgggattt				3761
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tattttttcac ttgttgcccc aaatgtgaaa gcatttcatt cttttaagag gcctaactca				4241
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ccaccagac atctgactaa tggctctgtg ccacactcc aagacctgtg ctttttagag				4361
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tttgtttaca tgatgaaact ttttgttggt gcttgtttgt atataataca atgtgtacat				4481
gtatcttttt ctcgattcaa atcttaaccc ttaggactct ggtatttttg atctggcaac				4541
catatttctg gaagttgaga tgtttcagct tgaagaacca aaacagaagg aatatgtaca				4601
aagaataaat tttctgctca cgatgagttt agtgtgtaaa gtttagagac atctgacttt				4661
gatagctaaa ttaaaccaaa ccctattgaa gaattgaata tatgtactt caagaaacta				4721
aattgatctc gtagaattat cttaataaaa taatggctat aatttctctg caaaatcaga				4781
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aatgtgggtt ctacatt				4858

<210> 476
 <211> 1056
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> 869
 <223> Xaa = Any Amino Acid

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 Lys Asn Ile Gln Val Val Val Arg Cys Arg Pro Phe Asn Leu Ala Glu
 20 25 30
 Arg Lys Ala Ser Ala His Ser Ile Val Glu Cys Asp Pro Val Arg Lys
 35 40 45
 Glu Val Ser Val Arg Thr Gly Gly Leu Ala Asp Lys Ser Ser Arg Lys
 50 55 60
 Thr Tyr Thr Phe Asp Met Val Phe Gly Ala Ser Thr Lys Gln Ile Asp
 65 70 75 80

Val	Tyr	Arg	Ser	Val	Val	Cys	Pro	Ile	Leu	Asp	Glu	Val	Ile	Met	Gly	
				85					90					95		
Tyr	Asn	Cys	Thr	Ile	Phe	Ala	Tyr	Gly	Gln	Thr	Gly	Thr	Gly	Lys	Thr	
			100					105					110			
Phe	Thr	Met	Glu	Gly	Glu	Arg	Ser	Pro	Asn	Glu	Glu	Tyr	Thr	Trp	Glu	
		115					120					125				
Glu	Asp	Pro	Leu	Ala	Gly	Ile	Ile	Pro	Arg	Thr	Leu	His	Gln	Ile	Phe	
	130				135						140					
Glu	Lys	Leu	Thr	Asp	Asn	Gly	Thr	Glu	Phe	Ser	Val	Lys	Val	Ser	Leu	
145					150					155					160	
Leu	Glu	Ile	Tyr	Asn	Glu	Glu	Leu	Phe	Asp	Leu	Leu	Asn	Pro	Ser	Ser	
			165						170					175		
Asp	Val	Ser	Glu	Arg	Leu	Gln	Met	Phe	Asp	Asp	Pro	Arg	Asn	Lys	Arg	
			180					185					190			
Gly	Val	Ile	Ile	Lys	Gly	Leu	Glu	Glu	Ile	Thr	Val	His	Asn	Lys	Asp	
		195					200					205				
Glu	Val	Tyr	Gln	Ile	Leu	Glu	Lys	Gly	Ala	Ala	Lys	Arg	Thr	Thr	Ala	
	210					215					220					
Ala	Thr	Leu	Met	Asn	Ala	Tyr	Ser	Ser	Arg	Ser	His	Ser	Val	Phe	Ser	
225					230					235					240	
Val	Thr	Ile	His	Met	Lys	Glu	Thr	Thr	Ile	Asp	Gly	Glu	Glu	Leu	Val	
			245						250					255		
Lys	Ile	Gly	Lys	Leu	Asn	Leu	Val	Asp	Leu	Ala	Gly	Ser	Glu	Asn	Ile	
			260					265					270			
Gly	Arg	Ser	Gly	Ala	Val	Asp	Lys	Arg	Ala	Arg	Glu	Ala	Gly	Asn	Ile	
		275					280					285				
Asn	Gln	Ser	Leu	Leu	Thr	Leu	Gly	Arg	Val	Ile	Thr	Ala	Leu	Val	Glu	
	290					295					300					
Arg	Thr	Pro	His	Val	Pro	Tyr	Arg	Glu	Ser	Lys	Leu	Thr	Arg	Ile	Leu	
305					310					315					320	
Gln	Asp	Ser	Leu	Gly	Gly	Arg	Thr	Arg	Thr	Ser	Ile	Ile	Ala	Thr	Ile	
			325						330					335		
Ser	Pro	Ala	Ser	Leu	Asn	Leu	Glu	Glu	Thr	Leu	Ser	Thr	Leu	Glu	Tyr	
			340					345					350			
Ala	His	Arg	Ala	Lys	Asn	Ile	Leu	Asn	Lys	Pro	Glu	Val	Asn	Gln	Lys	
		355					360					365				
Leu	Thr	Lys	Lys	Ala	Leu	Ile	Lys	Glu	Tyr	Thr	Glu	Glu	Ile	Glu	Arg	
	370					375					380					
Leu	Lys	Arg	Asp	Leu	Ala	Ala	Ala	Arg	Glu	Lys	Asn	Gly	Val	Tyr	Ile	
385					390					395					400	
Ser	Glu	Glu	Asn	Phe	Arg	Val	Met	Ser	Gly	Lys	Leu	Thr	Val	Gln	Glu	
			405						410					415		
Glu	Gln	Ile	Val	Glu	Leu	Ile	Glu	Lys	Ile	Gly	Ala	Val	Glu	Glu	Glu	
			420					425					430			
Leu	Asn	Arg	Val	Thr	Glu	Leu	Phe	Met	Asp	Asn	Lys	Asn	Glu	Leu	Asp	
		435					440					445				
Gln	Cys	Lys	Ser	Asp	Leu	Gln	Asn	Lys	Thr	Gln	Glu	Leu	Glu	Thr	Thr	
	450					455					460					
Gln	Lys	His	Leu	Gln	Glu	Thr	Lys	Leu	Gln	Leu	Val	Lys	Glu	Glu	Tyr	
465					470					475					480	
Ile	Thr	Ser	Ala	Leu	Glu	Ser	Thr	Glu	Glu	Lys	Leu	His	Asp	Ala	Ala	
			485						490					495		
Ser	Lys	Leu	Leu	Asn	Thr	Val	Glu	Glu	Thr	Thr	Lys	Asp	Val	Ser	Gly	
			500					505					510			
Leu	His	Ser	Lys	Leu	Asp	Arg	Lys	Lys	Ala	Val	Asp	Gln	His	Asn	Ala	
		515					520					525				
Glu	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Asn	Leu	Asn	Ser	Leu	Phe	Asn	Asn	
	530					535					540					
Met	Glu	Glu	Leu	Ile	Lys	Asp	Gly	Ser	Ser	Lys	Gln	Lys	Ala	Met	Leu	
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Glu	Val	His	Lys	Thr	Leu	Phe	Gly	Asn	Leu	Leu	Ser	Ser	Ser	Val	Ser	
			565						570					575		
Ala	Leu	Asp	Thr	Ile	Thr	Thr	Val	Ala	Leu	Gly	Ser	Leu	Thr	Ser	Ile	
			580					585					590			
Pro	Glu	Asn	Val	Ser	Thr	His	Val	Ser	Gln	Ile	Phe	Asn	Met	Ile	Leu	
		595					600					605				
Lys	Glu	Gln	Ser	Leu	Ala	Ala	Glu	Ser	Lys	Thr	Val	Leu	Gln	Glu	Leu	

610	Ile Asn Val Leu Lys Thr	615	Asp Leu Leu Ser Ser	620	Leu Glu Met Ile Leu
625	Ser Pro Thr Val Val Ser	630	Ile Leu Lys Ile Asn	635	Ser Gln Leu Lys His
	645		650		655
Ile Phe Lys Thr Ser Leu Thr Val Ala Asp Lys Ile Glu Asp Gln Lys	660	665		670	
Lys Glu Leu Asp Gly Phe Leu Ser Ile Leu Cys Asn Asn Leu His Glu	675	680		685	
Leu Gln Glu Asn Thr Ile Cys Ser Leu Val Glu Ser Gln Lys Gln Cys	690	695		700	
Gly Asn Leu Thr Glu Asp Leu Lys Thr Ile Lys Gln Thr His Ser Gln	705	710		715	720
Glu Leu Cys Lys Leu Met Asn Leu Trp Thr Glu Arg Phe Cys Ala Leu	725	730		735	
Glu Glu Lys Cys Glu Asn Ile Gln Lys Pro Leu Ser Ser Val Gln Glu	740	745		750	
Asn Ile Gln Gln Lys Ser Lys Asp Ile Val Asn Lys Met Thr Phe His	755	760		765	
Ser Gln Lys Phe Cys Ala Asp Ser Asp Gly Phe Ser Gln Glu Leu Arg	770	775		780	
Asn Phe Asn Gln Glu Gly Thr Lys Leu Val Glu Glu Ser Val Lys His	785	790		795	800
Ser Asp Lys Leu Asn Gly Asn Leu Glu Lys Ile Ser Gln Glu Thr Glu	805	810		815	
Gln Arg Cys Glu Ser Leu Asn Thr Arg Thr Val Tyr Phe Ser Glu Gln	820	825		830	
Trp Val Ser Ser Leu Asn Glu Arg Glu Gln Glu Leu His Asn Leu Leu	835	840		845	
Glu Val Val Ser Gln Cys Cys Glu Ala Ser Ser Ser Asp Ile Thr Glu	850	855		860	
Lys Ser Asp Gly Xaa Lys Ala Ala His Glu Lys Gln His Asn Ile Phe	865	870		875	880
Leu Asp Gln Met Thr Ile Asp Glu Asp Lys Leu Ile Ala Gln Asn Leu	885	890		895	
Glu Leu Asn Glu Thr Ile Lys Ile Gly Leu Thr Lys Leu Asn Cys Phe	900	905		910	
Leu Glu Gln Asp Leu Lys Leu Asp Ile Pro Thr Gly Thr Thr Pro Gln	915	920		925	
Arg Lys Ser Tyr Leu Tyr Pro Ser Thr Leu Val Arg Thr Glu Pro Arg	930	935		940	
Glu His Leu Leu Asp Gln Leu Lys Arg Lys Gln Pro Glu Leu Leu Met	945	950		955	960
Met Leu Asn Cys Ser Glu Asn Asn Lys Glu Glu Thr Ile Pro Asp Val	965	970		975	
Asp Val Glu Glu Ala Val Leu Gly Gln Tyr Thr Glu Glu Pro Leu Ser	980	985		990	
Gln Glu Pro Ser Val Asp Ala Gly Val Asp Cys Ser Ser Ile Gly Gly	995	1000		1005	
Val Pro Phe Phe Gln His Lys Lys Ser His Gly Lys Asp Lys Glu Asn	1010	1015		1020	
Arg Gly Ile Asn Thr Leu Glu Arg Ser Lys Val Glu Glu Thr Thr Glu	1025	1030		1035	1040
His Leu Val Thr Lys Ser Arg Leu Pro Leu Arg Ala Gln Ile Asn Leu	1045	1050		1055	

<210> 477

<211> 919

<212> DNA

<213> Homo sapiens

<220>

<221> allele

<222> 420

<223> N is any

<400> 477

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gcgctgaaga	gccaacata					919

<210> 478

<211> 2533

<212> DNA

<213> Homo sapiens

<220>

<221> allele

<222> 416,836,1766

<223> N is any

<400> 478

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<210> 479

<211> 2550

<212> DNA

<213> Homo sapiens

<220>

<221> allele

<222> 442,862,1792

<223> n is any

<400> 479

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<210> 480

<211> 1103

<212> DNA

<213> Homo sapiens

<220>

<221> allele
 <222> 247,604
 <223> N is any

<400> 480

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<210> 481
 <211> 974
 <212> DNA
 <213> Homo sapiens

<220>

<221> allele
 <222> 247
 <223> n is any

<400> 481

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<210> 482
 <211> 2493
 <212> DNA
 <213> Homo sapiens

<220>

<221> allele
 <222> 86,107,2149
 <223> n is any

<400> 482

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<210> 483

<211> 6012

<212> DNA

<213> Homo sapiens

<400> 483

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<221> allele

<222> 49, 59, 119, 249, 498, 718, 767, 898, 1156, 1174, 1500, 1512, 1892, 2220

<223> n = A,T,C or G

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Met Arg Ala Leu Leu Ala Arg Leu Leu Cys Val
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Leu Val Xaa Ser Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro
15 20 25

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Ser Asn Cys Asp Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr
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Phe Ser Asn Ile His Trp Cys Asn Cys Pro Lys Lys Phe Xaa Gly Gln
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cac tgt gaa ata gat aag tca aaa acc tgc tat gag ggg aat ggt cac 304
His Cys Glu Ile Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His
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Leu	Ala	Leu	*													
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<220>
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 <222> 15, 58, 141, 214, 231, 274, 366
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Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys					
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Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu					
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Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys					
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